



# Blast 2 Sequences results

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Taxonomy

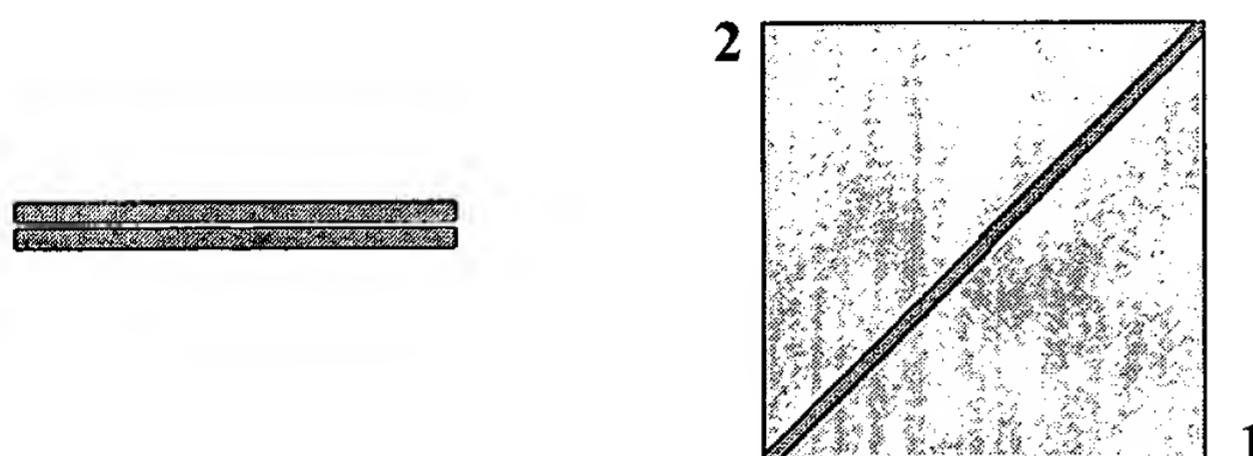
Structure

## BLAST 2 SEQUENCES RESULTS VERSION BLASTP 2.2.4 [Aug-26-2002]

Matrix **BLOSUM62** ▼ gap open: **11** gap extension: **1**  
**x\_dropoff:** **50** **expect:** **10.00** **wordsize:** **3** **Filter**  **Align**

**Sequence 1** gi 6746554 10-deacetylbaccatin III-10-O-acetyl transferase [Taxus cuspidata] **Length** 440 (1 .. 440)

**Sequence 2** gi 18034655 10-deacetylbaccatin III-10-O-acetyl transferase [Taxus baccata] **Length** 440 (1 .. 440)



NOTE: The statistics (bitscore and expect value) is calculated based on the size of nr database

Score = 857 bits (2215), Expect = 0.0  
 Identities = 430/440 (97%), Positives = 432/440 (97%)



Query: 1 MAGSTEFVVRSLERVMVAPSQSPPKAFLQLSTLDNLPGVRENIFNTLLVYNASDRVSVDP 60  
 MAGSTE VVRSLERVMVAPSQSPPKAFLQLSTLDNLPGVRENIFNTLLVYNASDRVSVDP

Sbjct: 1 MAGSTESVVRSLERVMVAPSQSPPKAFLQLSTLDNLPGVRENIFNTLLVYNASDRVSVDP 60

Query: 61 AKVIHQALSKVLVYYSPFAGRLRKENGDLVECTGEGALFVEAMADTDLSVLGDLDDYS 120  
 AKVIHQALSKVLVYYSPFAGRLRKENGDLVECTGEGALFVEAMADTDLSVLGDLDDYS

Sbjct: 61 AKVIHQALSKVLVYYSPFAGRLRKENGDLVECTGEGALFVEAMADTDLSVLGDLDDYS 120

Query: 121 PSLEQLLFCCLPPDTDIEDIHPLVVQVTRFTCGGFVVGVSFCHGICDGLGAGQFLIAMGEM 180  
 PSLEQLLFCCLPPDTDIEDIHPLVVQVTRFTCGGFVVGVSFCHGICDGLGAGQFLIAMGEM

Sbjct: 121 PSLEQLLFCCLPPDTDIEDIHPLVVQVTRFTCGGFVVGVSFCHGICDGLGAGQFLIAMGEM 180

Query: 181 ARGEIKPSSEPIWKRELLKPEDPLYRFQYYHFQLICPPSTFGKIVQGSILVITSETINCIK 240  
 ARGEIKPSSEPIWKRELLKPEDPLYRFQYYHF+LI PPSTFGKIVQGSIL ITSETI IK

Sbjct: 181 ARGEIKPSSEPIWKRELLKPEDPLYRFQYYHFRLIRPPSTFGKIVQGSILGITSETIKWIK 240

Query: 241 QCLREESKEFCSAFEVVSALAWIARTRALQIPHSENVKLIFAMDMRKLFPPLSKGYYGN 300  
 QCLREESKEFCSAFEVVSALAWIARTRALQIPHSENVKLIFAMDMRKLFPPL KGYYGN

Sbjct: 241 QCLREESKEFCSAFEVVSALAWIARTRALQIPHSENVKLIFAMDMRKLFPPLKGYYGN 300

Query: 301 FVGTVCAMDNVKDLLSGSLLRVVRIIKKAKVSLNEHFTSTIVTPRSGSDESINYENIVGF 360  
 FVGTVCAMDNVKDLLSGSLLRVVRIIKKAKVSLNEHFTSTIVTP SGSDESINYENIVGF

Sbjct: 301 FVGTVCAMDNVKDLLSGSLLRVVRIIKKAKVSLNEHFTSTIVTPCSGSDESINYENIVGF 360

Query: 361 GDRRLGFDEVDFGWHADNVSLVQHGLKDVSQSYFLFIRPPKNPDGIKILSFMP 420  
 GDRRLGFDEVDFGWHADNVSLVQHGLKDVSQSYFLFIRPPKNPDGIKILSFMP

Sbjct: 361 GDRRLGFDEVDFGWHADNVSLVQHGLKDVSQSYFLFIRPPKNPDGIKILSFMP 420

Query: 421 IVKSFKFEMETMTNKYVTKP 440  
 I+KSFKFEMETMTNKYVTKP

Sbjct: 421 IMKSFKFEMETMTNKYVTKP 440

CPU time: 0.08 user secs. 0.03 sys. secs 0.11 total secs.

Lambda K H  
0.321 0.139 0.414

Gapped

Lambda K H  
0.267 0.0410 0.140

Matrix: BLOSUM62

Gap Penalties: Existence: 11, Extension: 1

Number of Hits to DB: 1809

Number of Sequences: 0

Number of extensions: 119

Number of successful extensions: 1

Number of sequences better than 10.0: 1

Number of HSP's better than 10.0 without gapping: 1

Number of HSP's successfully gapped in prelim test: 0

Number of HSP's that attempted gapping in prelim test: 0

Number of HSP's gapped (non-prelim): 1

length of query: 440

length of database: 414,047,803

effective HSP length: 129

effective length of query: 311

effective length of database: 414,047,674

effective search space: 128768826614

effective search space used: 128768826614

T: 9

A: 40

X1: 16 ( 7.4 bits)

X2: 129 (49.7 bits)

X3: 129 (49.7 bits)

S1: 41 (21.9 bits)

S2: 76 (33.9 bits)